

## **Sequencing Ancient British Genomes Dr Matthew Teasdale**

The Appleby Archaeology Group's November talk was given by Dr Matthew Teasdale, recently of the Institute of Genetics at Trinity College Dublin and now at BioArCh, University of York. Dr Teasdale's subject was the sequencing of ancient British Genomes.

Matthew began by explaining how genome research can benefit archaeology by providing evidence of where distinct individuals and populations of ancient peoples originated, by determining and comparing mutations in ancient DNA recovered from human remains unearthed at archaeological sites. Such advances have been made possible largely by the drastic reduction in the costs of sequencing and also the exponential growth in computing power over the last 10-12 years. In 2004/5, the cost of sequencing a single genome was somewhere around US\$10 million, in 2017 the same can be achieved for US\$1000 - 2000. It is now even possible for any individual with £79 to have their own genome sequenced to look at his or her own ancestral geographic origins.

Another advantage of DNA sequencing in archaeological research is that it can be cross referenced with Carbon14 dating, which is by now a long established method of obtaining dating evidence from organic remains.

Matthew went on to describe the methodology of analysing an ancient genome. The technique uses mitochondrial DNA recovered from human bone, preferentially the petrosal bone just above the ear. This is because this bone is one of the most dense in the human body and thus contains many more cells for a given sample size. The bone sample is broken down into individual proteins and then into the cellular matrix from which the DNA is extracted. Mitochondrial DNA is found in both men and women and is used in preference to nuclear DNA, primarily because it evolves much faster, being directly inherited by an individual from the mother. In addition, a large number of copies of the genome are found in a single cell, unlike nuclear DNA, which contains just one. Finally, it is very well conserved within the cell over time.

Matthew continued his talk by explaining the practical application of ancient DNA sequencing on which he had been working while in Dublin. The team of which he had been a part had been investigating the migratory history of British populations, which typically had previously been examined using mainly archaeological methods, such as artefacts, including grave goods, differing burial practices, inscriptions and texts. In order to apply the new techniques to a similar range of individuals, they took samples from seven male genomes from a Roman context, dated between the 4<sup>th</sup> and 7th Centuries, which had been excavated in 2004-5 from a cemetery in York. In total, the remains of 82 males had been identified at the site, all aged between 19 and 45, over half of whom had been beheaded, so the cemetery was generally thought to have contained burials of either gladiators or criminals. In addition, the team included DNA from an iron age woman from Yorkshire,

dated circa 100BC and an Anglo-Saxon man from County Durham, circa 800AD. These samples were compared to a large database of genomic information from modern populations.

The findings proved to be extremely interesting. All the individual samples revealed mitochondrial genomes common in modern European populations and showed that of the seven males buried within a Roman context, most were found to belong to a North Western European grouping and to have a close genetic resemblance with a modern Welsh, ie. a native British population, rather than those from Yorkshire. The mitochondrial DNA from the iron age female showed a similar pattern, whilst that from the Anglo-Saxon male most resembled that of modern East Anglian and Dutch people, confirming the influx of a Germanic population during the post-Roman occupation. Analysis of the 'Y' DNA (which is only inherited by males from their fathers) of remains in the Roman context confirmed the Western European origin, with one exception. The single sample which didn't fit the same pattern showed an individual belonging to a Middle Eastern grouping – study of isotopes in his teeth confirmed differences in the location of his early upbringing from that of his companions, who were, broadly speaking, brought up in and around the Vale of York.

Matthew ended his talk by referring to the enormous potential of ancient DNA sequencing in the investigation of movements of particular individuals and how this would enable us to see more clearly the lives of our distant ancestors.

After taking questions, Matthew was warmly thanked by the audience.

The next talk in the series will be on 14<sup>th</sup> December, when the subject will be Digital Archaeology.